

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/574,306A
Source: IFWP
Date Processed by STIC: 3/15/07

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IFWP

RAW SEQUENCE LISTING

DATE: 03/15/2007

PATENT APPLICATION: US/10/574,306A

TIME: 15:06:51

Input Set : A:\50458.002001.txt

Output Set: N:\CRF4\03152007\J574306A.raw

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3 <110> APPLICANT: Korherr, Christian
5 <120> TITLE OF INVENTION: Medical Use of TBK-1 or of Inhibitors Thereof
7 <130> FILE REFERENCE: 50458/002001
9 <140> CURRENT APPLICATION NUMBER: US 10/574,306A
10 <141> CURRENT FILING DATE: 2006-04-03
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010996
13 <151> PRIOR FILING DATE: 2004-10-01
15 <150> PRIOR APPLICATION NUMBER: US 60/508,100
16 <151> PRIOR FILING DATE: 2003-10-02
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3031
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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30 taacaagagg attgcctgat ccagccaaga tgcagagcac ttctaatacat ctgtggcttt      120
32 tatctgatat tttaggccaa ggagctactg caaatgtctt tctgtggaaga cataagaaaa      180
34 ctggtgattt atttgcctatc aaagtattta ataacataag cttccttcgt ccagtggatg      240
36 ttcaaagtga agaatttgaa gtgttgaaaa aactcaatca caaaaatatt gtcaaattat      300
38 ttgctattga agaggagaca acaacaagac ataaagtact tattatggaa ttttgtccat      360
40 gtgggagttt atacactgtt ttagaagaac cttctaatagc ctatggacta ccagaatctg      420
42 aattcttaat tgttttgcca gatgtggtgg gtggaatgaa tcatctacga gagaatggtg      480
44 tagtgcaccg tgatatcaag ccaggaaata tcatgcgtgt tataggggaa gatggacagt      540
46 ctgtgtacaa actcacagat tttggtgcag ctagagaatt agaagatgat gagcagtttg      600
48 tttctctgta tggcacagaa gaatatattgc accctgatat gtatgagaga gcagtgtctaa      660
50 gaaaagatca tcagaagaaa tatggagcaa cagttgatct ttggagcatt ggggtaacat      720
52 tttaccatgc agctactgga tcaactgcat ttagaccctt tgaagggcct cgtaggaata      780
54 aagaagtgat gtataaaata attacaggaa agccttcttg tgcaatatct ggagtacaga      840
56 aagcagaaaa tggaccaatt gactggagtg gagacatgcc tgtttcttgc agtctttctc      900
58 ggggtcttca ggttctactt acccctgttc ttgcaaacat ccttgaagca gatcaggaaa      960
60 agtggtgggg ttttgaccag ttttttgcag aaactagtga tatacttcac cgaatggtaa      1020
62 ttcattgttt ttcgctacaa caaatgacag ctcataagat ttatattcat agctataata      1080
64 ctgctactat atttcatgaa ctggtatata aacaaaccaa aattatttct tcaaatacaag      1140
66 aacttatcta cgaagggcga cgcttagtct tagaacctgg aaggctggca caacatttcc      1200
68 ctaaaactac tgaggaaaac cctatatattg tagtaagccg ggaacctctg aataccatag      1260
70 gattaatata tgaaaaaatt tccctcccta aagtacatcc acgttatgat ttagacgggg      1320
72 atgctagcat ggctaaggca ataacagggg ttgtgtgtta tgacctgaga attgccagta      1380
74 ccttactgct ttatcaggaa ttaatgcgaa aggggatacg atggctgatt gaattaatta      1440
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78 gtatcagaaa cattgaaaaa actgtgaaag tatatgaaaa gttgatgaag atcaacctgg      1560
80 aagcggcaga gttaggtgaa atttcagaca tacacaccaa attgttgaga ctttccagtt      1620

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82 ctcaggggaac aatagaaacc agtcttcagg ataatcgacag cagattatct ccaggtggat 1680
84 cactggcaga cgcattgggca catcaagaag gcactcatcc gaaagacaga aatgtagaaa 1740
86 aactacaagt cctgttaaat tgcattgacag agatttacta tcagttcaaa aaagacaaaag 1800
88 cagaacgtag attagcttat aatgaagaac aaatccacaa atttgataag caaaaactgt 1860
90 attaccatgc cacaaaagct atgacgcact ttacagatga atgtgttaaa aagtatgagg 1920
92 catttttgaa taagtcagaa gaatggataa gaaagatgct tcatcttagg aaacagttat 1980
94 tatcgctgac taatcagtgt tttgatattg aagaagaagt atcaaaatat caagaatata 2040
96 ctaatgagtt acaagaaact ctgcctcaga aaatgtttac agcttccagt ggaatcadac 2100
98 ataccatgac cccaatttat ccaagttcta acacattagt agaaatgact cttggtatga 2160
100 agaaattaaa ggaagagatg gaaggggtgg ttaaagaact tgctgaaaat aaccacattt 2220
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104 tttctaatag aagtttaaga aaagtttccg tttgcacaag aaaataacgc ttgggcatga 2340
106 aatgaatgcc tttatagata gtcacttggt tctacaattc agtattttgat gtggctcgtgt 2400
108 aaatatgtac aatattgtaa atacataaaa aatatacaaa tttttggctg ctgtgaagat 2460
110 gtaattttat cttttaacat ttataattat atgaggaaat ttgacctcag tgatcacgag 2520
112 aagaaagcca tgaccgacca atatgttgac atactgatcc tctactctga gtggggctaa 2580
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116 ccttacaat caggaagact gacttgacac gtttgtaaat ggtagaacgg tggctactgt 2700
118 gagtggggag cagaaccgca ccactgttat actgggataa caattttttt gagaaggata 2760
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124 tttttccttt ggccataaat gtgtaattgt cattaaaatt ctaaggtcat ttcaactgtt 2940
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128 ttttaattga aagaaaaaaa aaaaaaaaaa a 3031
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132 <211> LENGTH: 729
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
138 Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
139 1 5 10 15
142 Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
143 20 25 30
146 Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
147 35 40 45
150 Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
151 50 55 60
154 Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Thr Thr Arg
155 65 70 75 80
158 His Lys Val Leu Ile Met Glu Phe Cys Pro Cys Gly Ser Leu Tyr Thr
159 85 90 95
162 Val Leu Glu Glu Pro Ser Asn Ala Tyr Gly Leu Pro Glu Ser Glu Phe
163 100 105 110
166 Leu Ile Val Leu Arg Asp Val Val Gly Gly Met Asn His Leu Arg Glu
167 115 120 125
170 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Val
171 130 135 140
174 Ile Gly Glu Asp Gly Gln Ser Val Tyr Lys Leu Thr Asp Phe Gly Ala
175 145 150 155 160

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178 Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val Ser Leu Tyr Gly Thr
179          165          170          175
182 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
183          180          185          190
186 Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp Leu Trp Ser Ile Gly
187          195          200          205
190 Val Thr Phe Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Arg Pro Phe
191          210          215          220
194 Glu Gly Pro Arg Arg Asn Lys Glu Val Met Tyr Lys Ile Ile Thr Gly
195 225          230          235          240
198 Lys Pro Ser Gly Ala Ile Ser Gly Val Gln Lys Ala Glu Asn Gly Pro
199          245          250          255
202 Ile Asp Trp Ser Gly Asp Met Pro Val Ser Cys Ser Leu Ser Arg Gly
203          260          265          270
206 Leu Gln Val Leu Leu Thr Pro Val Leu Ala Asn Ile Leu Glu Ala Asp
207          275          280          285
210 Gln Glu Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp
211          290          295          300
214 Ile Leu His Arg Met Val Ile His Val Phe Ser Leu Gln Gln Met Thr
215 305          310          315          320
218 Ala His Lys Ile Tyr Ile His Ser Tyr Asn Thr Ala Thr Ile Phe His
219          325          330          335
222 Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln Glu Leu
223          340          345          350
226 Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu Ala Gln
227          355          360          365
230 His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val Ser Arg
231          370          375          380
234 Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser Leu Pro
235 385          390          395          400
238 Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met Ala Lys
239          405          410          415
242 Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser Thr Leu
243          420          425          430
246 Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu Ile Glu
247          435          440          445
250 Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr Glu Val
251          450          455          460
254 Val Ile Thr Leu Asp Phe Cys Ile Arg Asn Ile Glu Lys Thr Val Lys
255 465          470          475          480
258 Val Tyr Glu Lys Leu Met Lys Ile Asn Leu Glu Ala Ala Glu Leu Gly
259          485          490          495
262 Glu Ile Ser Asp Ile His Thr Lys Leu Leu Arg Leu Ser Ser Ser Gln
263          500          505          510
266 Gly Thr Ile Glu Thr Ser Leu Gln Asp Ile Asp Ser Arg Leu Ser Pro
267          515          520          525
270 Gly Gly Ser Leu Ala Asp Ala Trp Ala His Gln Glu Gly Thr His Pro
271          530          535          540
274 Lys Asp Arg Asn Val Glu Lys Leu Gln Val Leu Leu Asn Cys Met Thr

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275 545          550          555          560
278 Glu Ile Tyr Tyr Gln Phe Lys Lys Asp Lys Ala Glu Arg Arg Leu Ala
279          565          570          575
282 Tyr Asn Glu Glu Gln Ile His Lys Phe Asp Lys Gln Lys Leu Tyr Tyr
283          580          585          590
286 His Ala Thr Lys Ala Met Thr His Phe Thr Asp Glu Cys Val Lys Lys
287          595          600          605
290 Tyr Glu Ala Phe Leu Asn Lys Ser Glu Glu Trp Ile Arg Lys Met Leu
291          610          615          620
294 His Leu Arg Lys Gln Leu Leu Ser Leu Thr Asn Gln Cys Phe Asp Ile
295 625          630          635          640
298 Glu Glu Glu Val Ser Lys Tyr Gln Glu Tyr Thr Asn Glu Leu Gln Glu
299          645          650          655
302 Thr Leu Pro Gln Lys Met Phe Thr Ala Ser Ser Gly Ile Lys His Thr
303          660          665          670
306 Met Thr Pro Ile Tyr Pro Ser Ser Asn Thr Leu Val Glu Met Thr Leu
307          675          680          685
310 Gly Met Lys Lys Leu Lys Glu Glu Met Glu Gly Val Val Lys Glu Leu
311          690          695          700
314 Ala Glu Asn Asn His Ile Leu Glu Arg Phe Gly Ser Leu Thr Met Asp
315 705          710          715          720
318 Gly Gly Leu Arg Asn Val Asp Cys Leu
319          725
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323 <211> LENGTH: 19
324 <212> TYPE: RNA
325 <213> ORGANISM: artificial
327 <220> FEATURE:
328 <223> OTHER INFORMATION: oligonucleotide siTBK-1 sense
330 <400> SEQUENCE: 3
331 ggagacaaca acaagacau
334 <210> SEQ ID NO: 4
335 <211> LENGTH: 20
336 <212> TYPE: RNA
337 <213> ORGANISM: artificial
339 <220> FEATURE:
340 <223> OTHER INFORMATION: oligonucleotide siTBK-1 antisense
342 <400> SEQUENCE: 4
343 augucuuguu guugucuccc
346 <210> SEQ ID NO: 5
347 <211> LENGTH: 23
348 <212> TYPE: DNA
349 <213> ORGANISM: artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: oligonucleotide TBK-1 sense
354 <400> SEQUENCE: 5
355 ttgaagagga gacaacaaca aga
358 <210> SEQ ID NO: 6
359 <211> LENGTH: 19

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19

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360 <212> TYPE: DNA
361 <213> ORGANISM: artificial
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364 <223> OTHER INFORMATION: oligonucleotide TBK-1 antisense
366 <400> SEQUENCE: 6
367 cattccaccc accacatct 19
370 <210> SEQ ID NO: 7
371 <211> LENGTH: 20
372 <212> TYPE: DNA
373 <213> ORGANISM: artificial
375 <220> FEATURE:
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378 <400> SEQUENCE: 7
379 cttgccttgc tgctctacct 20
382 <210> SEQ ID NO: 8
383 <211> LENGTH: 20
384 <212> TYPE: DNA
385 <213> ORGANISM: artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: oligonucleotide VEGF antisense
390 <400> SEQUENCE: 8
391 gattctgccc tctccttct 20
394 <210> SEQ ID NO: 9
395 <211> LENGTH: 20
396 <212> TYPE: DNA
397 <213> ORGANISM: artificial
399 <220> FEATURE:
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406 <210> SEQ ID NO: 10
407 <211> LENGTH: 20
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409 <213> ORGANISM: artificial
411 <220> FEATURE:
412 <223> OTHER INFORMATION: oligonucleotide Rantes antisense
414 <400> SEQUENCE: 10
415 gcacttgcca ctggtgtaga 20

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY

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